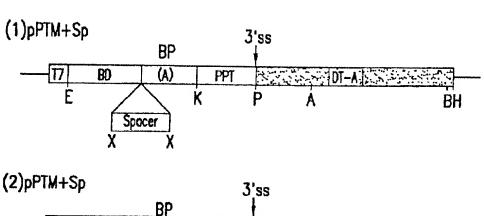
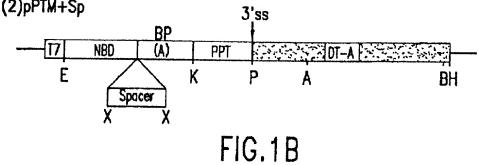


FIG.1A





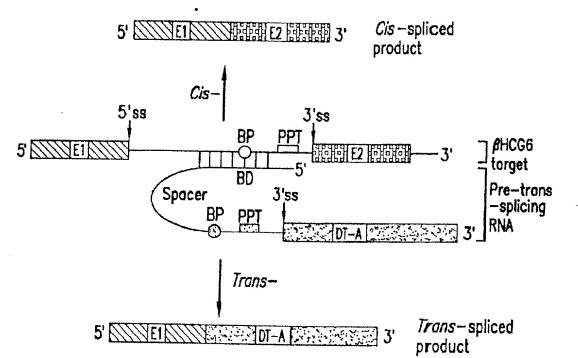
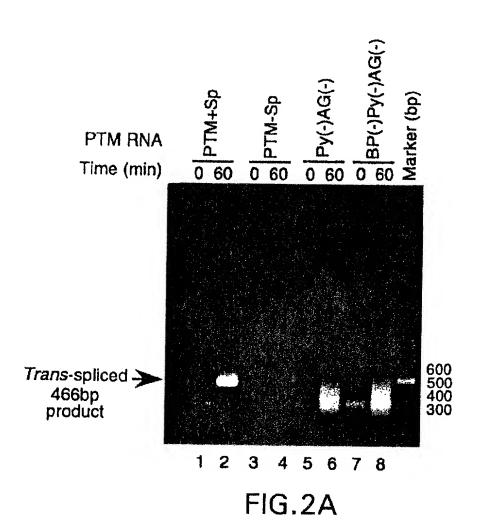


FIG.1C



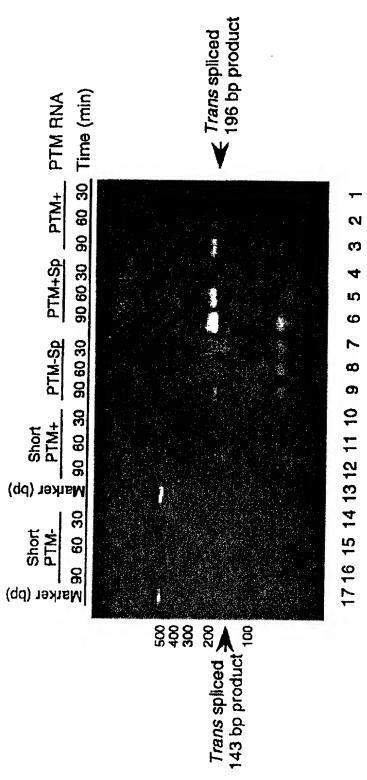


FIG.2B

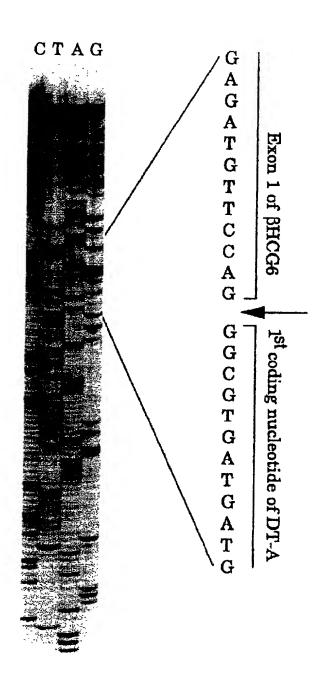


FIG.3

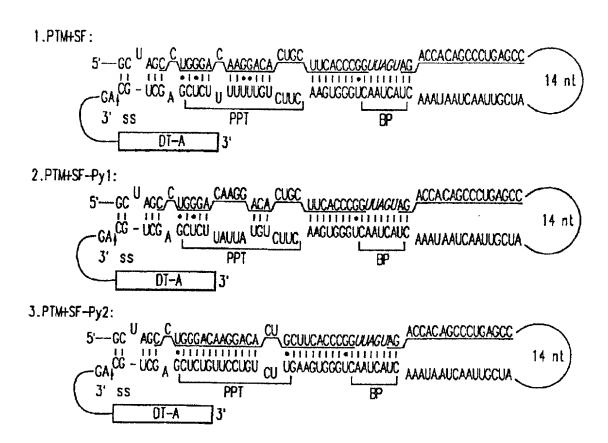


FIG.4A

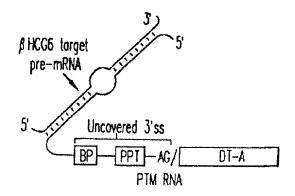
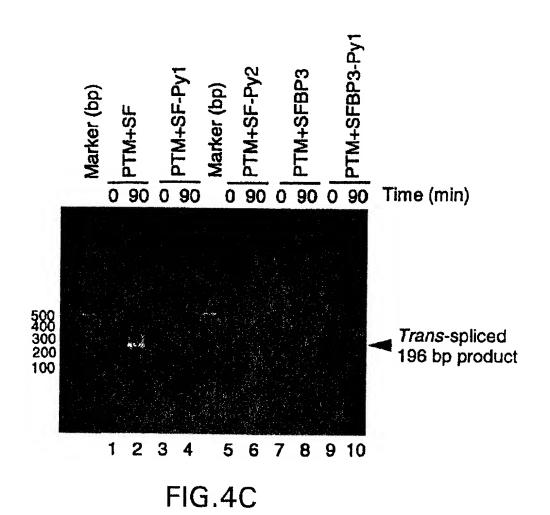
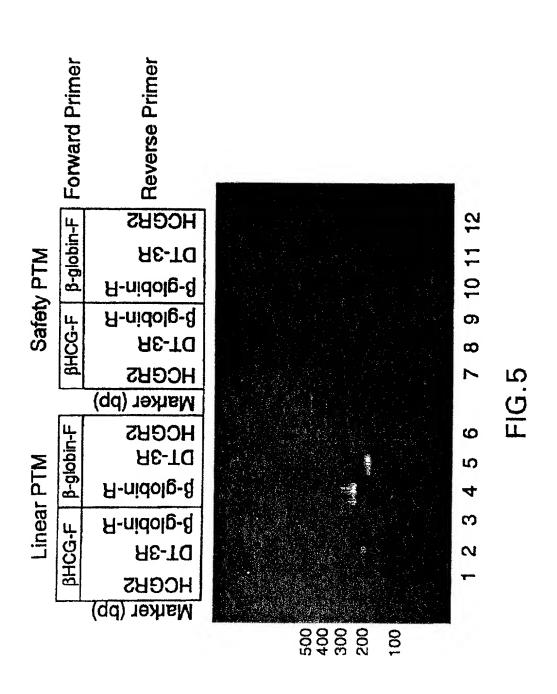
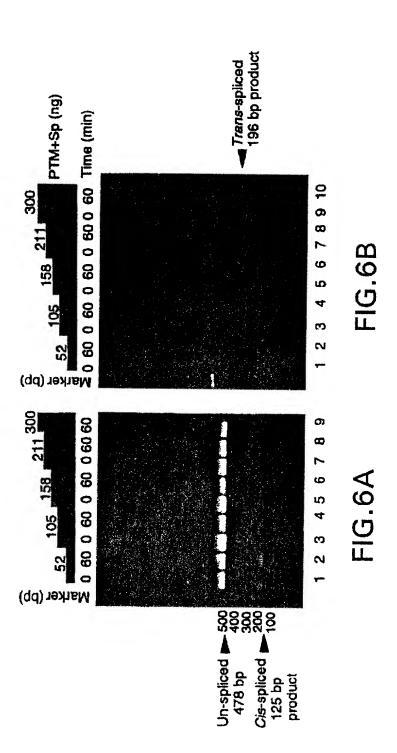
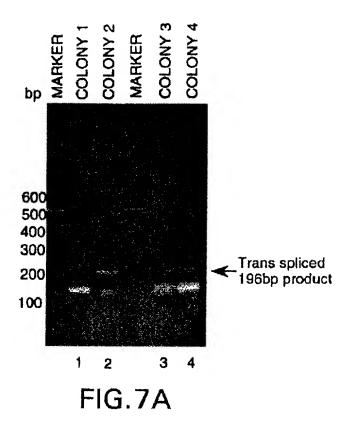


FIG.4B



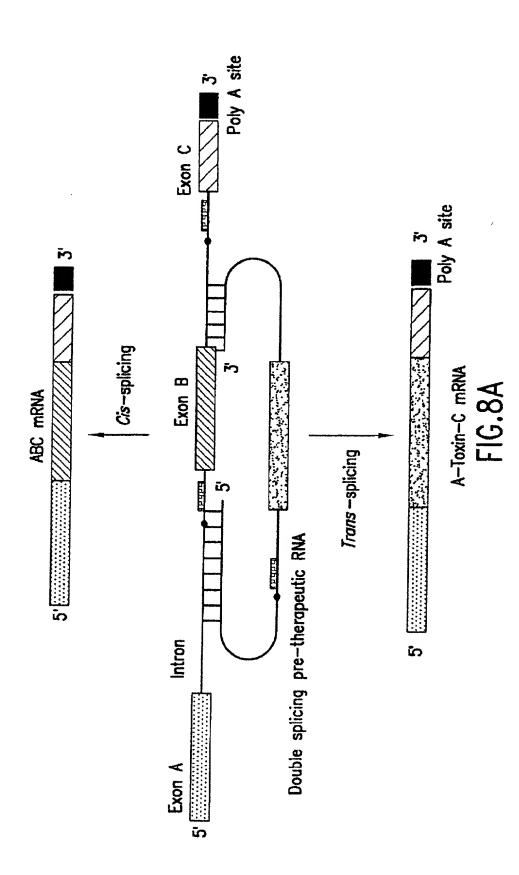




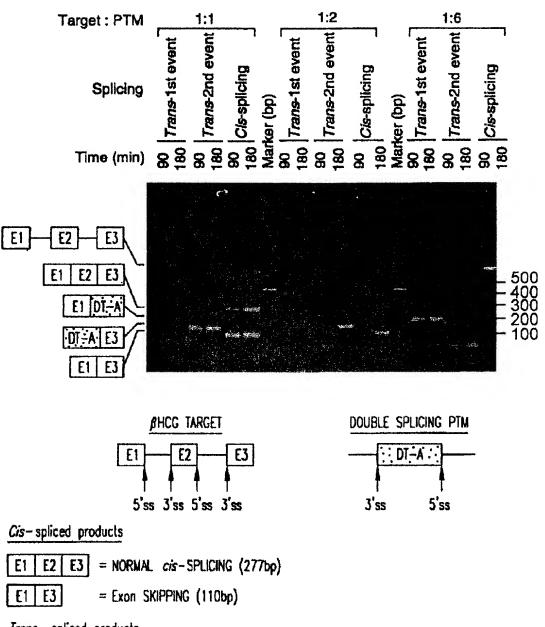


1ST CODING NUCLEOTIDE OF DT-A GATTCTTCTTAAATCTTTTGTGAAGAAACTTTTCTTCGTACCACGGGACTA EXON 1 OF PHOGE | 5-CAGGGGAGCACCAAGGATGTTCCAG-GGGGCTGATGATGTTGTT AACCTGGTTATGTAGATTCCATTCAAAA-3'

F16.7



h. 12



Trans- spliced products

E1 DT-A = 1st EVENT, 196bp. Trans-SPLICING BETWEEN 5' ss OF TARGET & 3' ss OF PTM.

DT-A E3 = 2nd EVENT, 161bp. Irans- SPLICING BETWEEN 3' ss OF TARGET & 5' ss OF PTM.

FIG.8B

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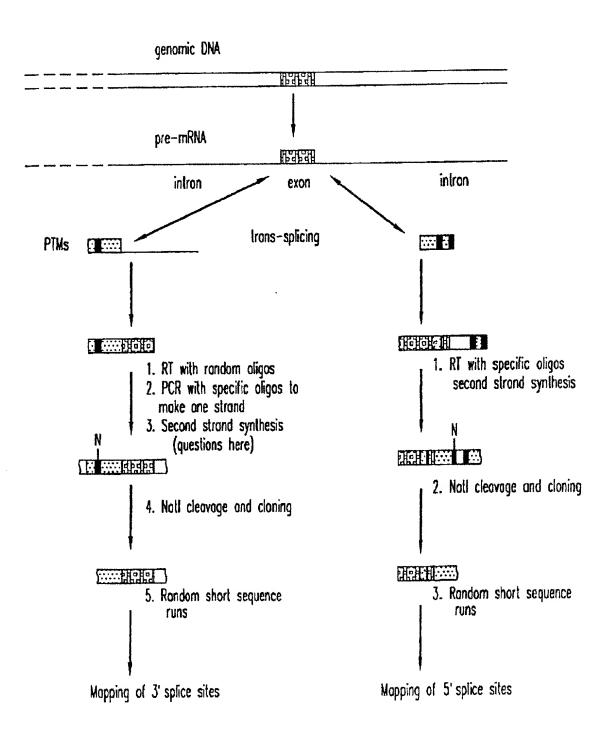
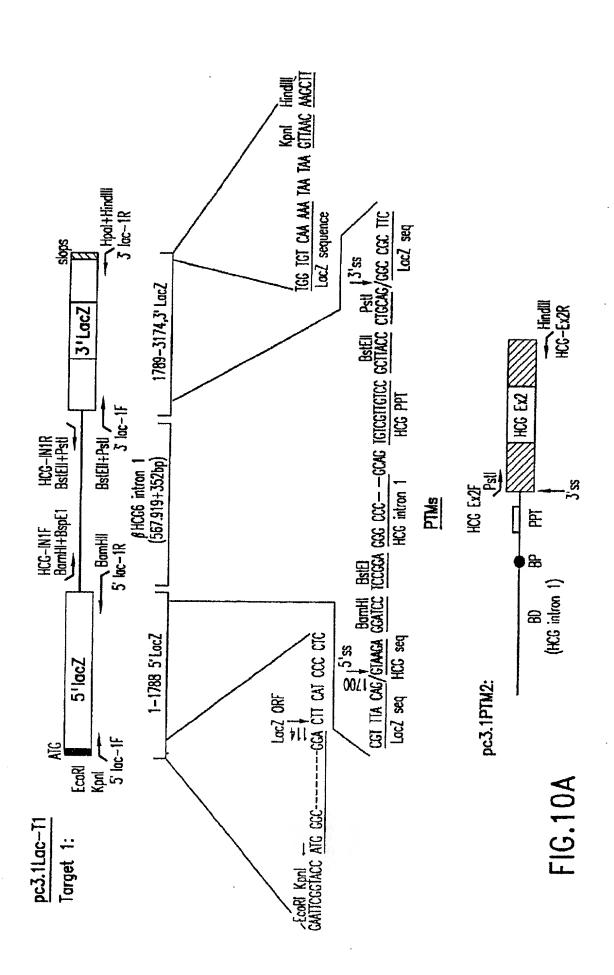


FIG.9



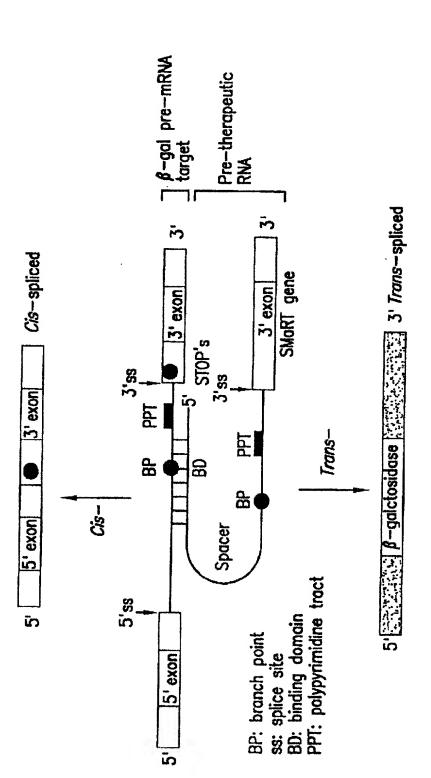
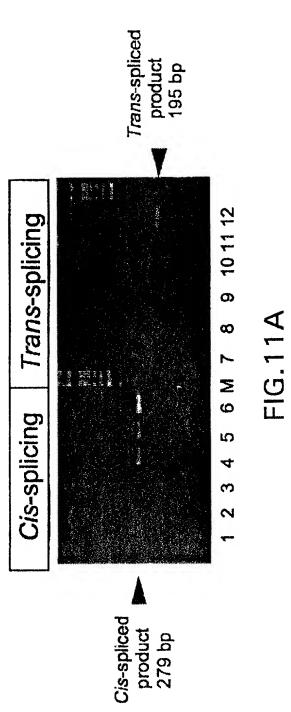


FIG. 10B



۲...

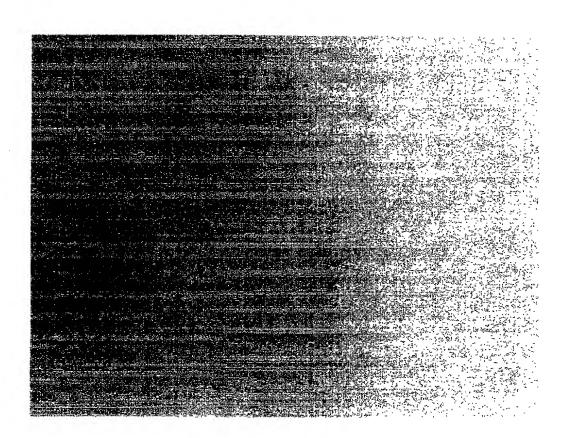


FIG.11B

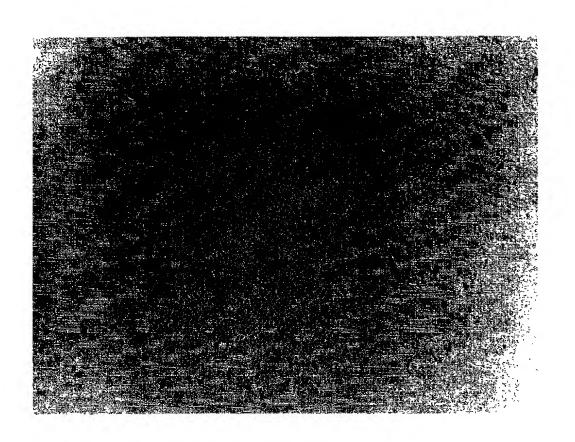


FIG.11C

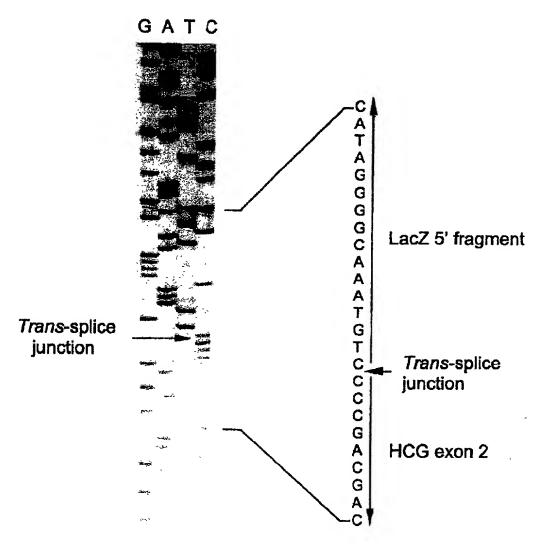


FIG.12A

1. NUCLEOTIDE SEQUENCES OF THE cis-SPLICED PRODUCT (285 bp):

BioLac-TR1

GCCTTTCCCTACCTGCACACACCCCCCCTGATCCTTTCCCAATACGCCCACGCCATGCGTAACACTCTTG

GOGGTTTCGCTAAATACTGGCAGGCGTTTCGTCAGTATCCCCGGTTTACAG/GGCGGCTTCGTCTAATAATG Splice junction

GGACTGGGTGGATCAGTGGCTGATTAAATATGATGAAAAGGGCAACCCGTGGTCGGCTTACGGCGGGTGATTT

TGGCCATACGCCCAACCAACCAGTTCTGTATGAACGGTCTGGTCTTTGCCCGACCGCCACCCCAG

2. NUCLEOTIDE SEQUENCES OF THE trans-SPLICED PRODUCT (195 bp)

BioLac-TR1

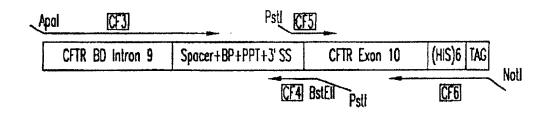
GGCTTTCGCTACCTGGAGAGGCGCCCCTGATCCTTTGCGAATACGCCCACGCGATGCGTAACACTCTTGC

Splice junction
CGGTTTCGCTAAATACTGCCAGGCGTTTCGTCAGTATCCCCGTTTACAG/GGGCTGCTGCTGCTGCTGCTGCT

GAGCATGGGCGGGACATGGGCATCCAAGGAGCCACTTCGGCCACGGGCCGC

FIG. 12B

CFTR Pre-therapeutic molecule (PTM or "bullet")



F.--

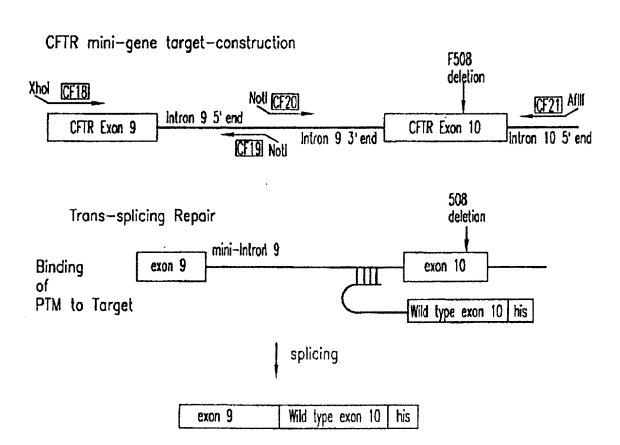


FIG.13

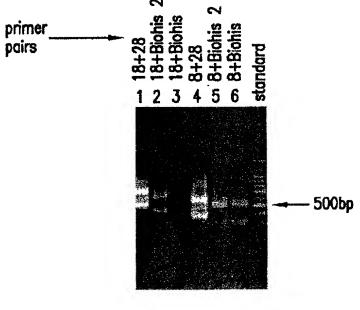


FIG.14

DNA sequence 500 b.p. GCTAGCGTTTAA ... TGCCACTCCCAC linear

Positions of Restriction Endonucleases sites (unique sites underlined)

TITITICCTGCACACTICACTICIAATGATGATTATGGGAGAGCTGGAGCCTTCAGAGGGTAAAAT 160 GCTAGCG TTTAAACGGGCCCACCATCATTATTAGGTCATTATCCCCGGAACATTATTATAACGTTGCTCCAGTACTAAC 80 ACCATGGAGAAGAAAAAAAGGACGTCTGAAGATGAAGATTACTACTAATACCCTCTTGACCTCGGAAGTCTCCCATTTTA CCATCCCAAATTTGCCCGGGTGGTAGTAATACCAGTAATAGCCGCTTGTAATATTGCAACGAGCTCATGATTG EXON 10 CFTR + HIS TAG + STOP Sca 1 BINDING DOMAIN INTRON 9 BD Dde I Sau96 Hae III Sau96 I Ban II Apg Xmn **IGETACCTCTTCTT** Dra I Kpn I

FIG.15A

GTGTTTCCTATGATGATATAGATACAGAAGCGTCATCAAAGCATGCCAACTAGAAGAGCATCATCATCATCATTAG 320

Sph I

190

CACAAAGGATACTACTTATATCTATGTCTTCGCAGTAGTTTCGTACGTTGATCTTCTCGTAGTAGTAGTAGTAGTAATC

| IAAGCACAGTGGAAGAATTTCATTCTGTTGTCAGTTTTCCTGGATTATGCCTGGCACCATTAAAGAAAATATCATCTTTG

ATTCGTGTCACCTTCTTAAAGTAAGACAAGAGTCAAAAGGACCTAATACGGACCGTGGTAATTTCTTTATAGTAGAAAC

Sac I Ban II	Sau3A I	Opn I Hind III	B <u>amH I</u> Kpn I I I I SACTAGTGGATCCSAGCTCGGTACC	CF28 17 384 399	390		378 PRESENT IN PTM 3' UT 378 BUT NOT TARGET				
			Not I ECOR V ECOR I	GCGCCGCCACTGTGCTGGATATCTGCCACAAATTCCACCACAC	CGCCGGCCGTGACACGACTATAGACGTCTTAAGGTGGTGTGAC	321 339 349	323 344			Sau3A i	ppn I

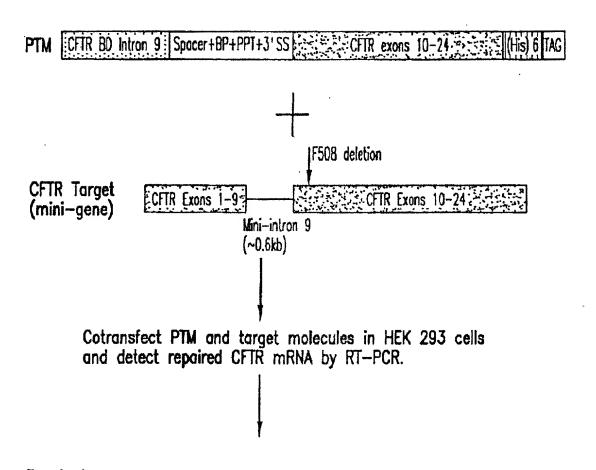
Ī

410 410

CTGGAAGGTGCCACTCCCAC 500 GACCTTCCACGGTGAGGGTG

	7	-	1		1	1	i
	Sau96 I	Sca 1	Sma 1	Sph 1	Sp. 1	Ssp I	Stu 1
nsage	1	•		i	7	1	3
Restriction Endonucleases site usage	lde I	the 1	lot I	FIM I	st I	Vu]	vu II
	-	-	1	2 F	1	-	1
	EcoR I	EcoR V	Hae II	Hoe III	Hing II	Hind III	Hinf I
Rest	1	***	1	1		7	1
	Acc I	Apa I	Apal I	Avr II	BamH 1	Ban II	Bbe I

1033616033



Repaired CFTR mRNA

Exons 10-24 CFTR CFTR Exons 1-9

FIG.16

Double Splicing PTM



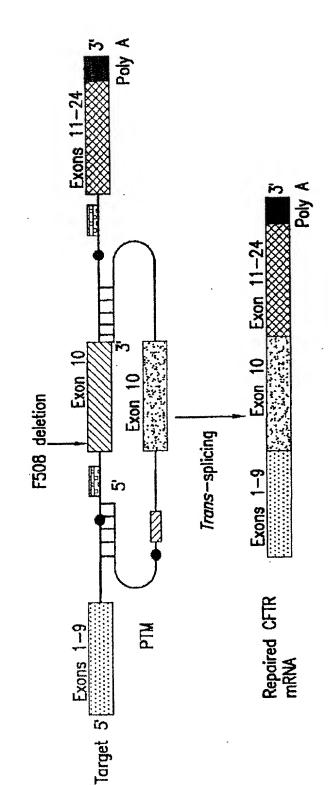
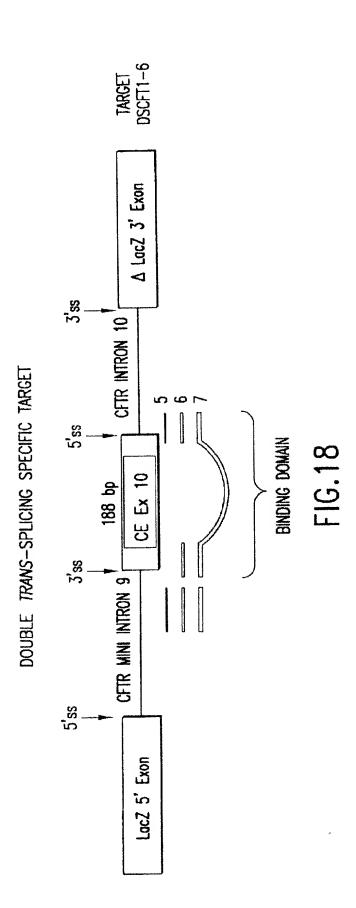


FIG.17



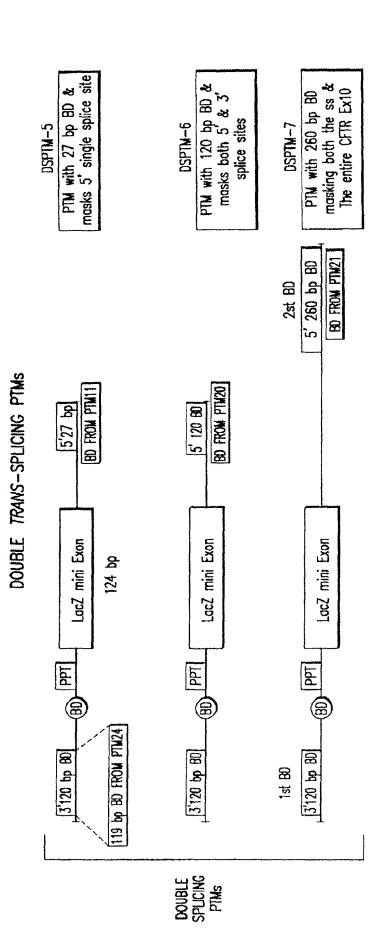
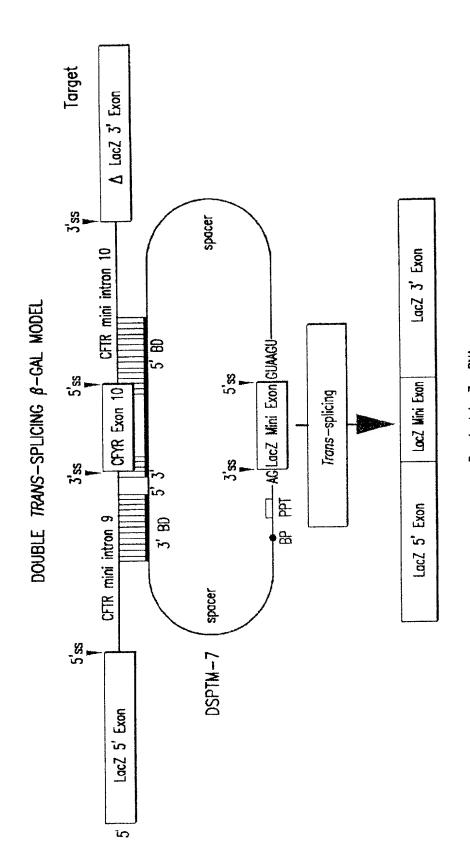
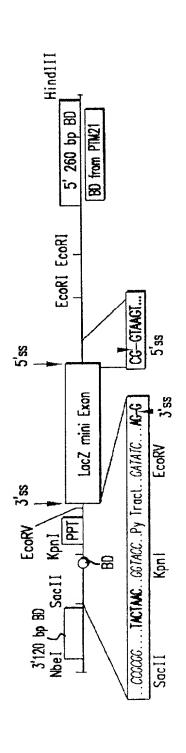


FIG. 19



Repaired LacZ mRNA FIG.20



(1) 3' BD (120 BP): GATICACTIGCICCAAITAICAICCIAAGCAGAAGIGIATATICITAITIGIAAAGAIICIATIAACICATTIGATIC AAAA1ATTTAAAA1ACTTCCTGTTTCATACTCTGCTATGCAC

(2) Spacer sequences (24 bp): AACATTATTATAACGTIGCTCGAA

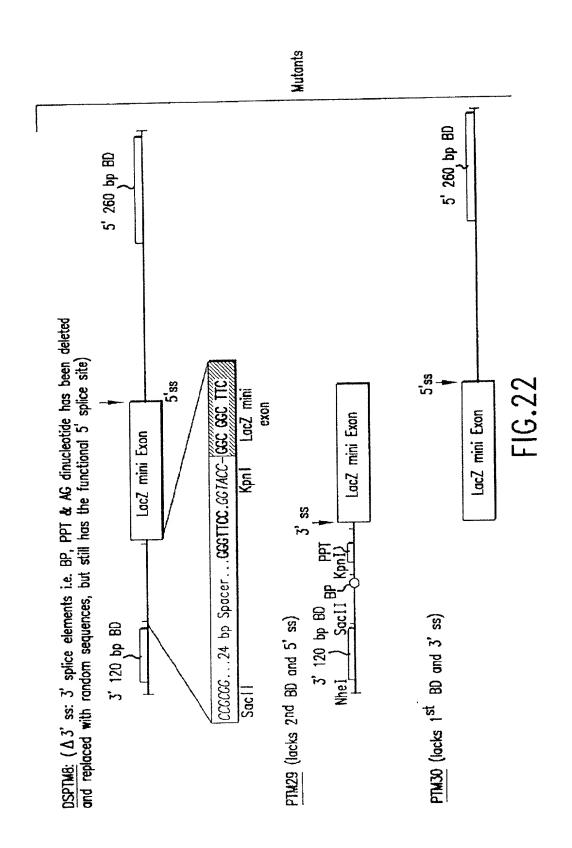
3'ss LacZ mini ★ exon BP Kpn | PPT EcoRV | ex (3) Branch point, pyrimidine tract and acceptor splice site: IACTAAC | GCTACC | CTICTITITITITITITITICATATC CTGCAG GGC GGC

(4) 5' donor site and 2nd spacer sequence: | IGA ACG|67AAG1 GTIATCACCCATATGTGTCTAACCTGATTCGGCCTTCGATACG LacZ mini 5'ss

CTAAGATCCACCGG

BD (260 BP): ICAAAAAGTITICACATAATTICTTACCICTICTIGAATTCAIGCTTIGATGACCTTCIGIATCIATATTCATCATIGGAA ACACCAATGATTTTTCTTTAATGGTGCCTGGCATAATCCTGGAAAACTGATAACAATGAAATTCTTCCACTGTGTGCTTAA AAAAACCCTCTGAA*TTC*TCCATTTCTCCCATAATCATCATTACAACTGAACTCTGGAAATAAAACCCATCATTATTAACTCA FTATCAAATCACG (2) 2,

FIG.21



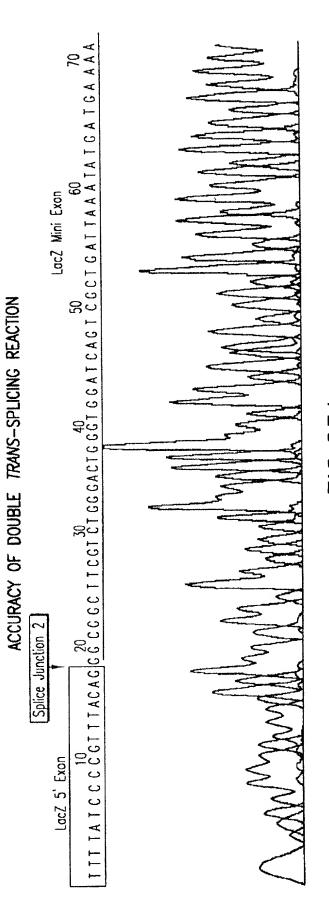


FIG.23A

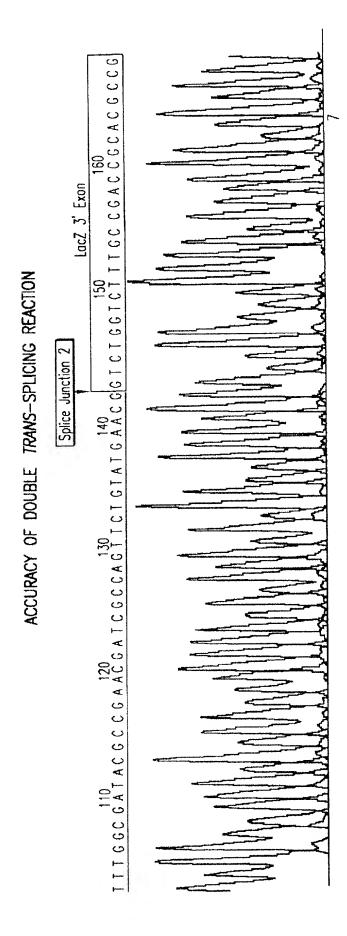


FIG.23B

Double Trans-splicing Produces Full-length Protein

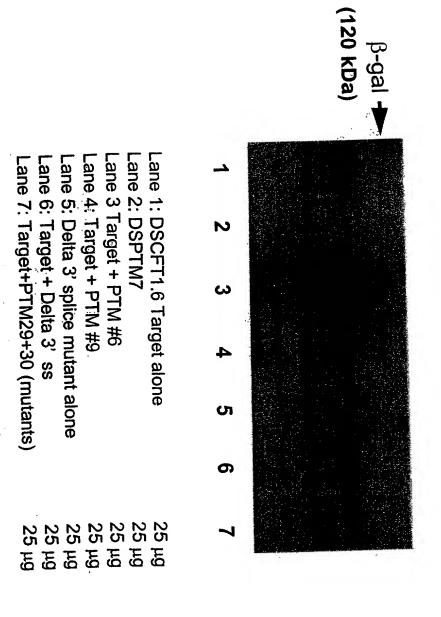
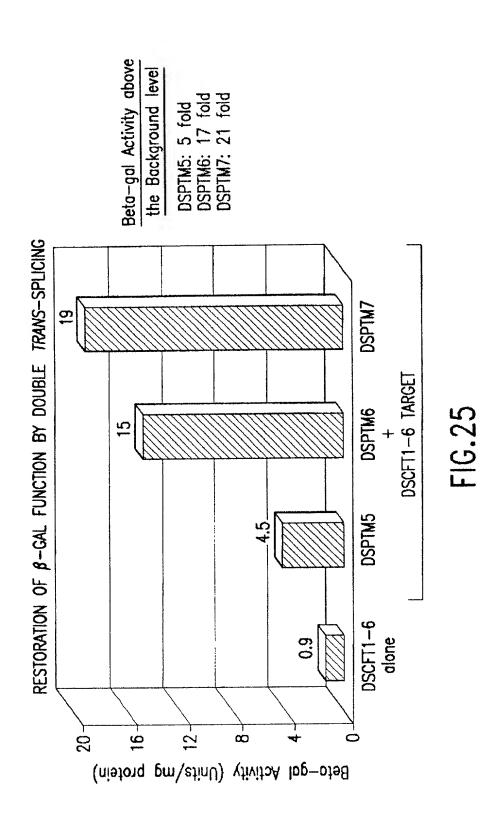


Figure 24



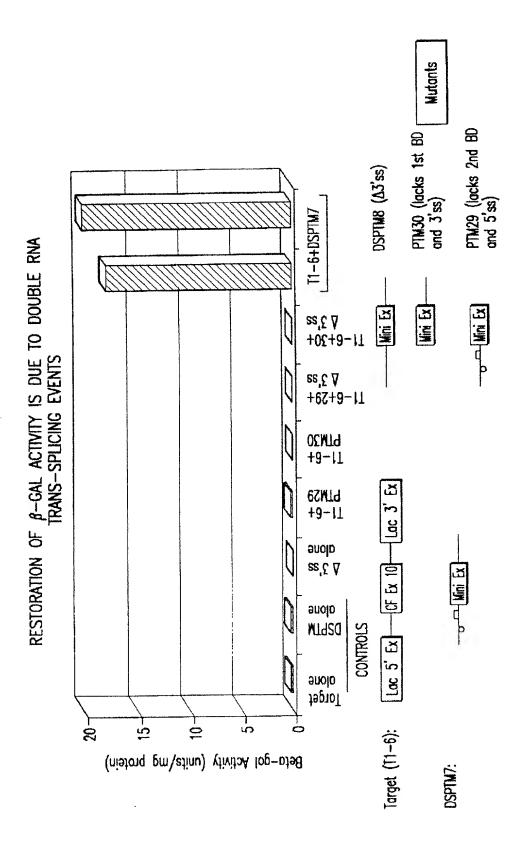


FIG. 2

QUALLIT PAICHI

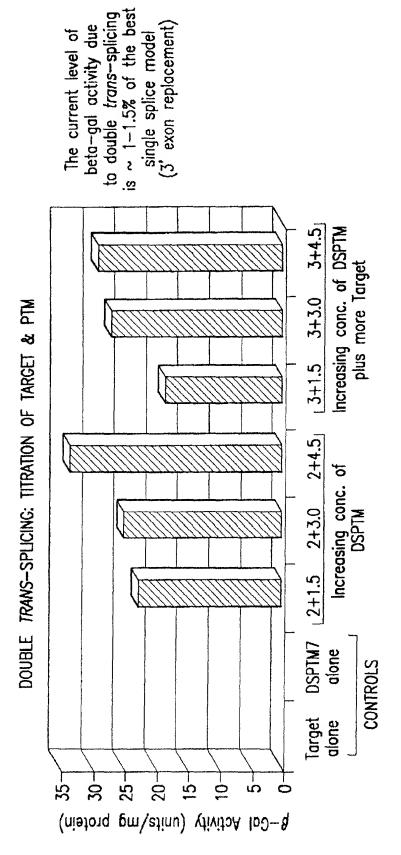
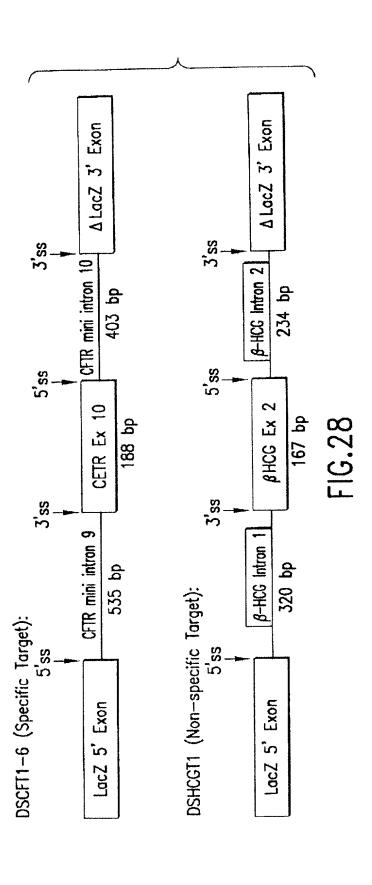


FIG.27



SPECIFICITY OF DOUBLE TRANS-SPLICING REACTION

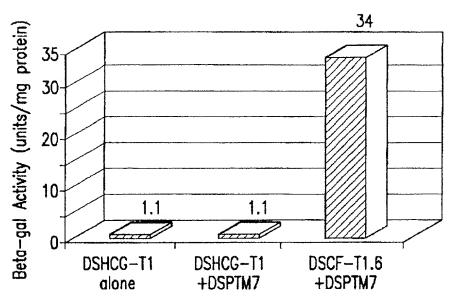


FIG.29

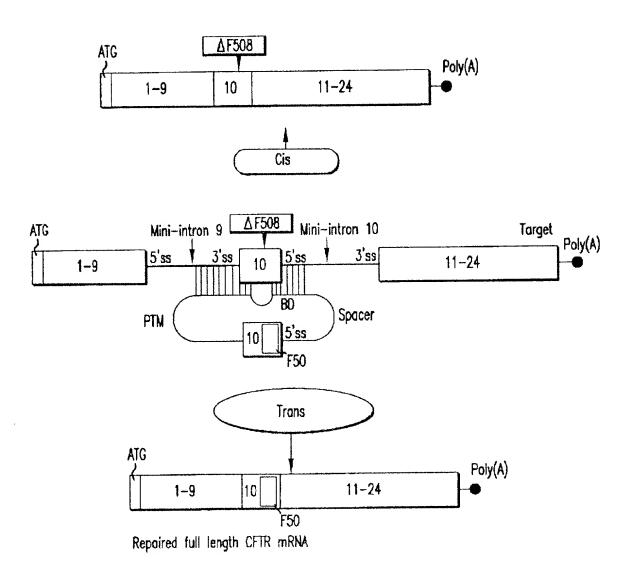
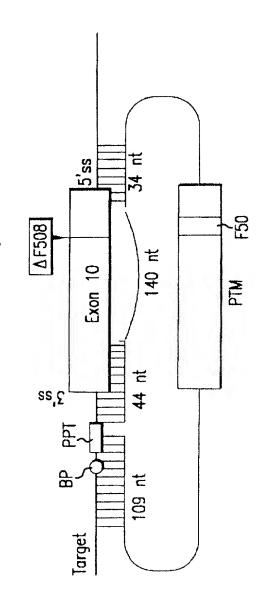


FIG.30

PTM with a long binding domain masking two splice sites and part of exon 10 in a mini-gene target



GCCGCATCAGCTTTTGCAGCCAATTCAGTTGGATCATGCCCCGGTACCATCAAGGAGAAGATAAT CTTCGCCGTCAGTTACGACGAGTACCGCTATCGCTCGGTGATTAAGGCCTTCAGTTGGAGGAG A<u>CGAGCT</u>TGCTCATGATGATGATGGGCCGAGTTAGAACCAAGTGAAGGCAAGATCAAACATTCCG

MCU in exon 10 of PTM 88 OF 192 (46%) bases in PTM exon 10 are not complementary to its binding domain (bold and underlined).

FIG. 3

Sequence of a double Trans—spliced product

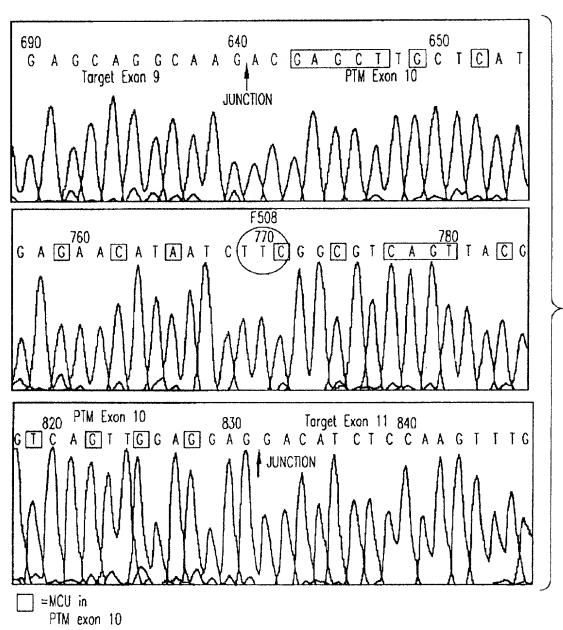
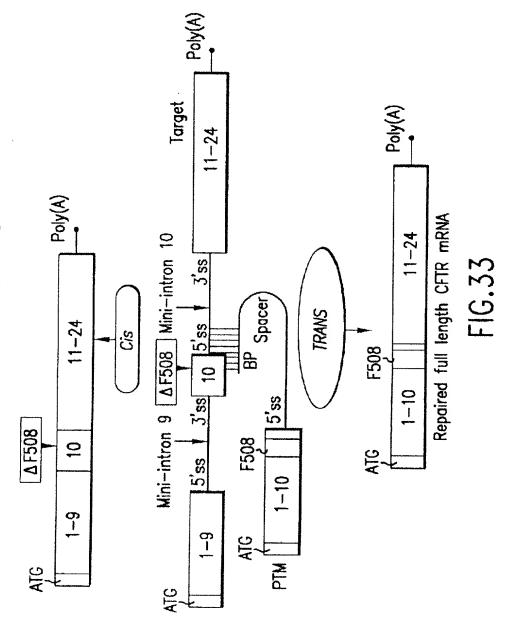


FIG.32

CF—TR Repair: 5' Exon—Replacement schematic diagram of a PTM binding to the splices site of intron 10 of a mini—gene target



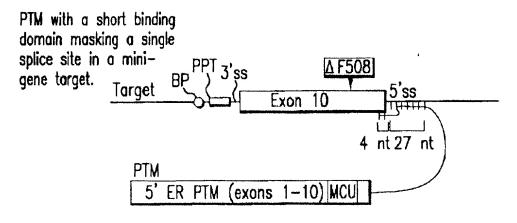


FIG.34A

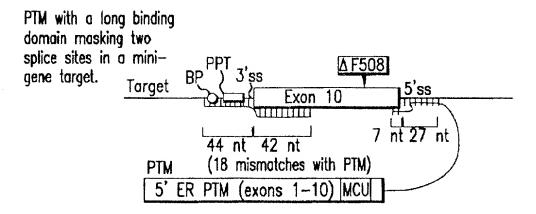


FIG.34B

PTM with a long binding domain masking two splice sites and the whole of exon 10 in a mini-gene target.

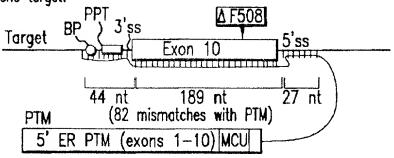
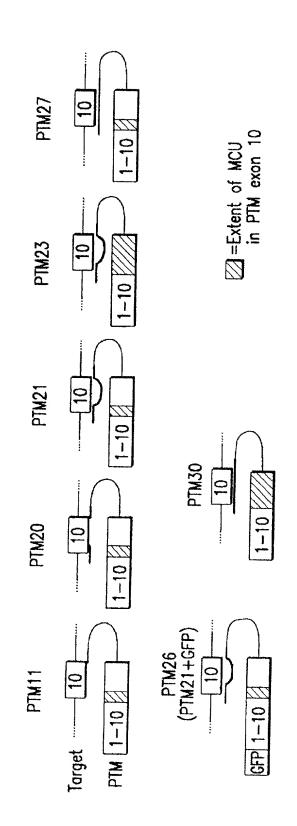


FIG.34C

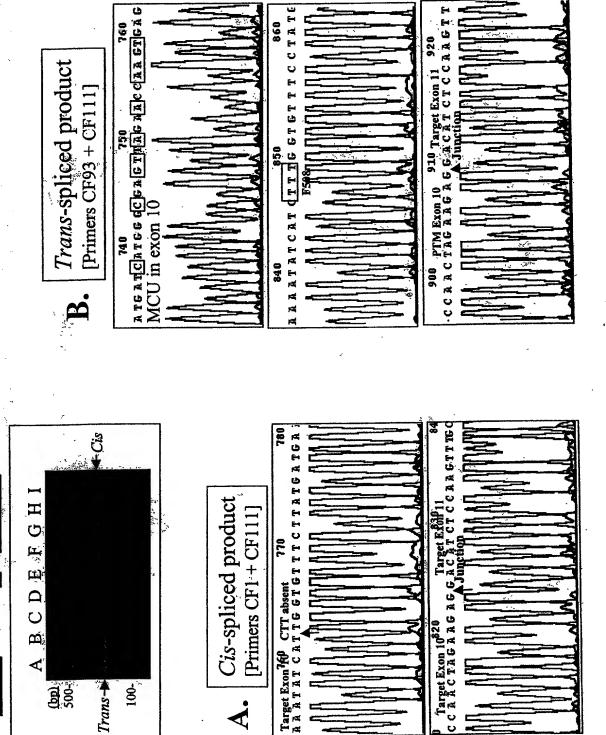


MCU in exon 10 of PTM 88 of 192 (46%) bases in PTM exon 10 are not complemetary to its binding domain.

ACCAGCTTGCTCATGATGATGATGGGGGTTAGAACCAAGTGAAGGGAGGATCAAACATTCCG GCCGCATCAGCTTTTGCAGCCAATTCAGTTGGATCATGCCCGGGTACCATCAAGGAGAAGATAAT CTTGGGGTCAGTTAGGAGGAGTACCGTTTGGCTOGGTGATTAAGGCCTGTCAGTTGGAGGAG

FIG. 3.

Target



48 mugit

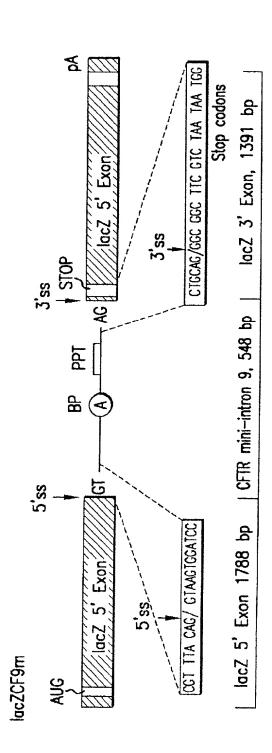


FIG.37A

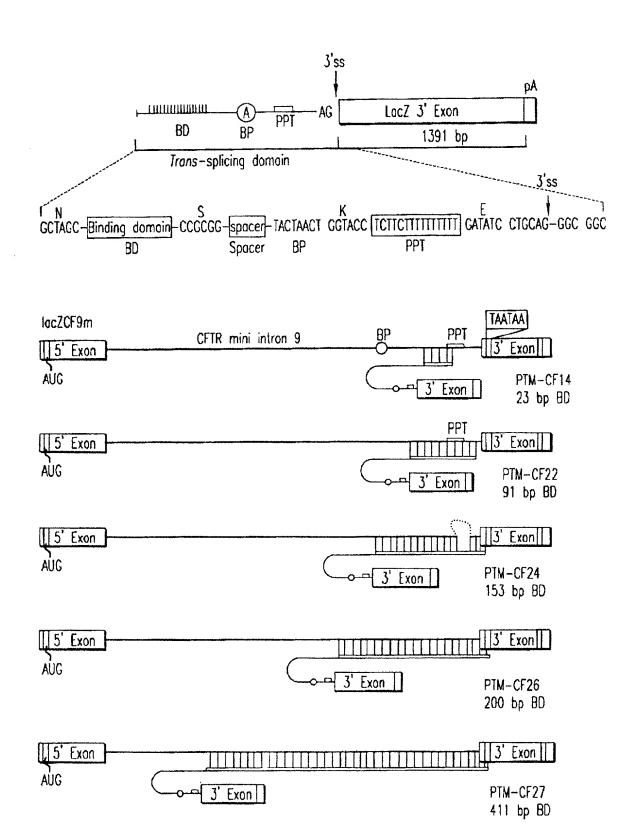
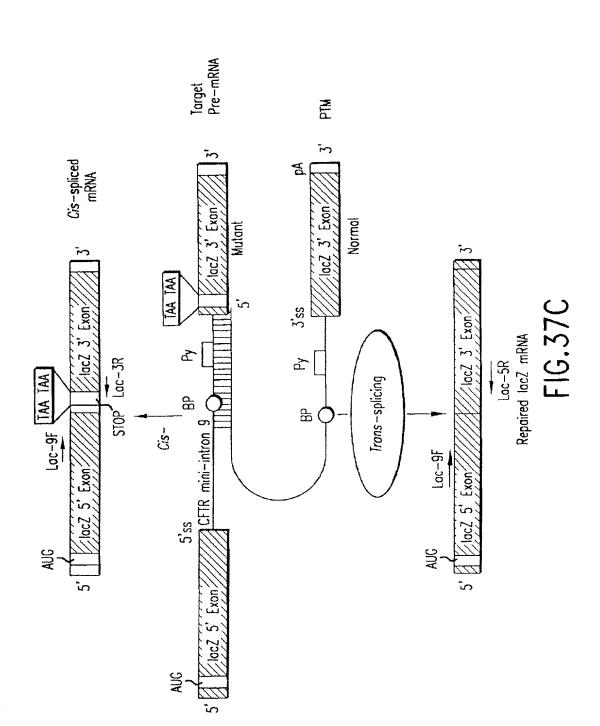
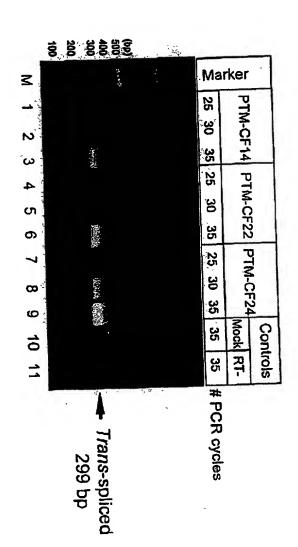


FIG.37B





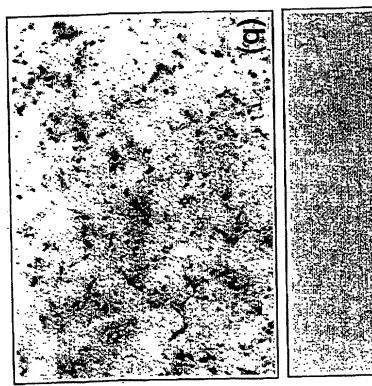
Š.

W

Figure 38B

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PAGE, 20



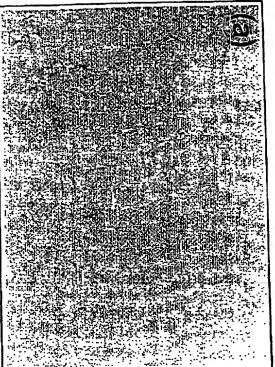
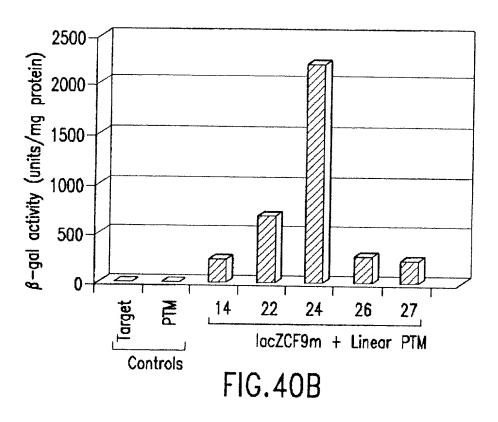
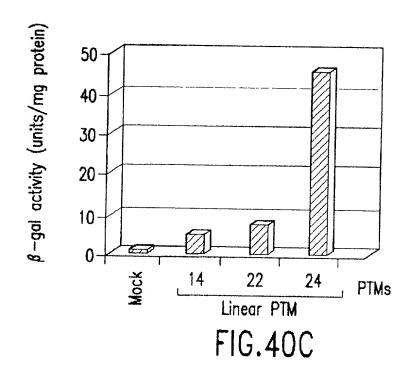


Figure 40A





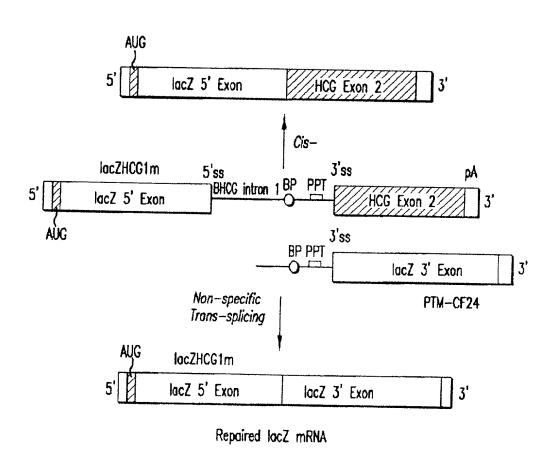
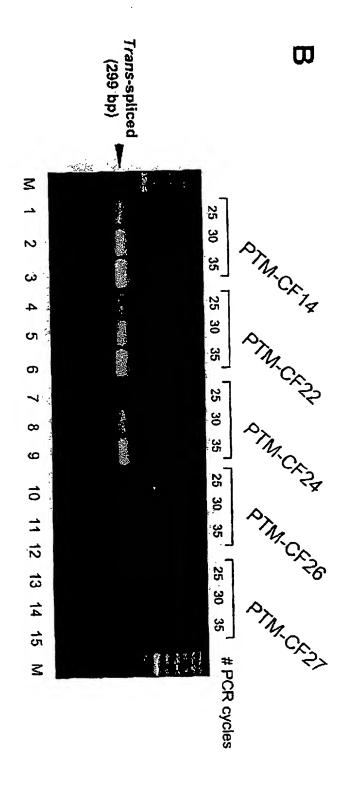


FIG.41A



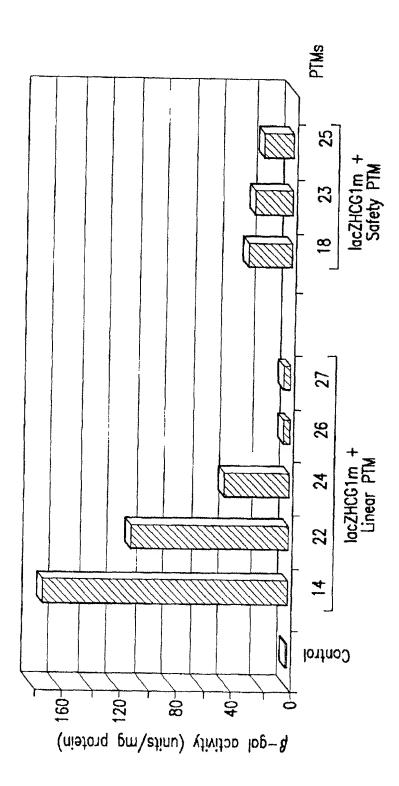


FIG.41C

153 bp PTM24 Binding Domain:

Nhe I

CCTAGC—MATAATGACCAAGCCGCCCCTCACGCTCAGGATTCACTTGCCTCCAATTATCATCCTAAGCAGAAGTGTATA

TICTTATTTGTAAAGATTCTATTAACTCATTTGATTCAAAATATTTAAAATACTTCCTGTTTCACCTACTCTGCTATGC

Sac II

FIG.43A

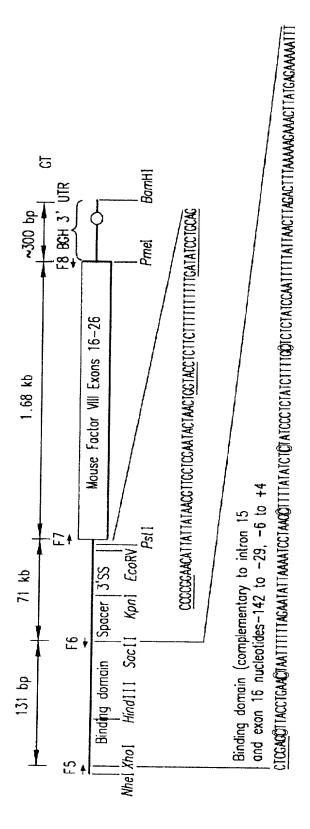


FIG. 44A

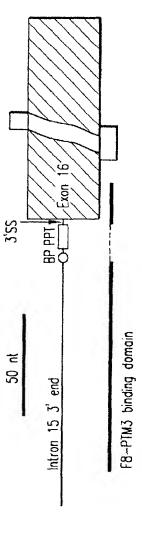


FIG.44B

Chicken &-actin

Promoter

Nucleotide changes are shown in blue Boxed=Cat box, TATA box
Boxed+Arrow=Transcription Start
Oval=Downstream elements
Bold=Binding domain
Italicized=Spacer+PPT+BP+AG dinucleotide

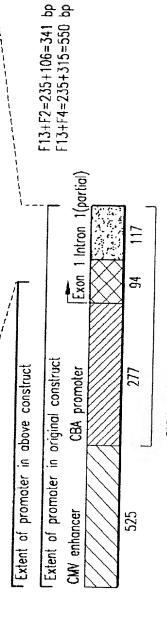


FIG. 44C

Chicken Beta Actin Promoter (including exan 1 and part of intron 1)

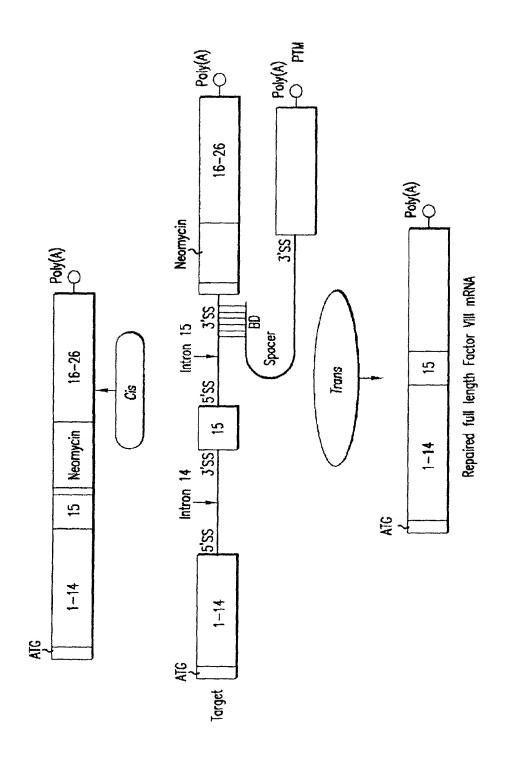
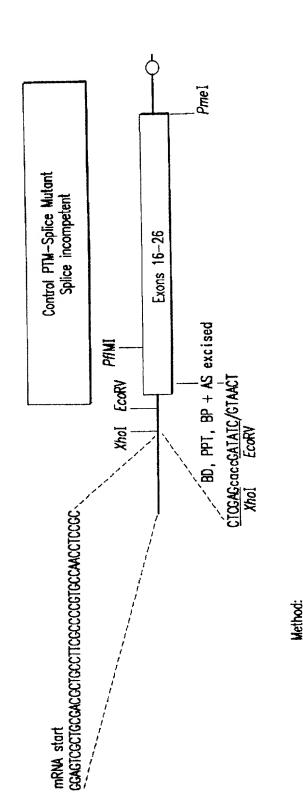


FIG.44[



FIC A

Excise TSD and part of exon 16 with XhoI and PfIMI and ligate in a PCR product that:
1) eliminates the TSD and splice acceptor site
2) inserts EcoRV adjacent to exon 16
3) restores the coding for exon 16

Repair of Factor VIII Preliminary results from one experiment

FVIII activity in Exon 16 FVII-KO mice after IV PTM-FVII intraportal infusion $(100 \mu gDNA)(n=3)$

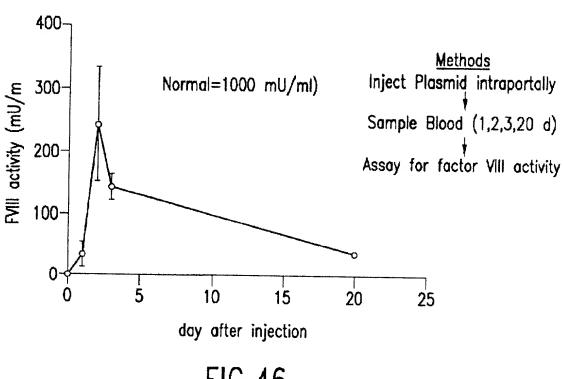


FIG.46

Detailed structure of a mouse factor VIII PTM containing normal sequences for exons 16—26 and a C—terminal FLAG tag. BGH=bovine growth hormone 3' UTR; Binding domain= 125 bp.

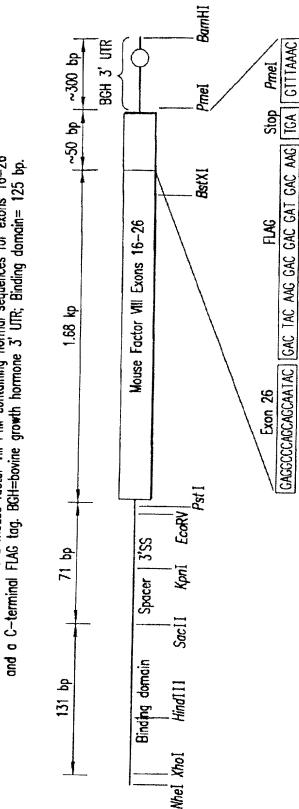
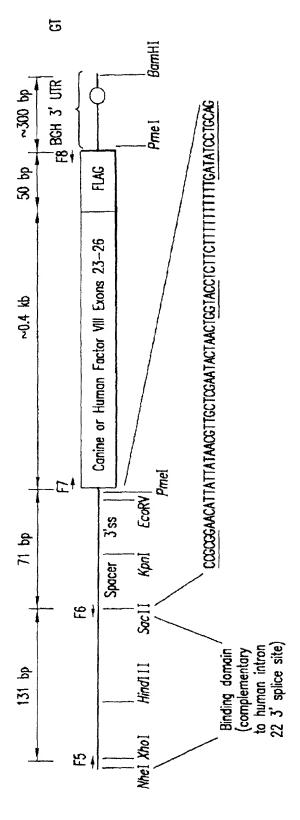


FIG.47A



FLAG=C—terminal tag to be used to detect repaired factor VIII protein.

FIG. 471